

1653

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/553,368

DATE: 05/09/2000
TIME: 16:38:51

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\05092000\I553368.raw

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ENTERED

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Ill, Charles R. et al.
7 (ii) TITLE OF INVENTION: NOVEL VECTORS AND GENES EXHIBITING
8 INCREASED EXPRESSION
10 (iii) NUMBER OF SEQUENCES: 11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
14 (B) STREET: 28 STATE STREET
15 (C) CITY: BOSTON
16 (D) STATE: MASSACHUSETTS
17 (E) COUNTRY: US
18 (F) ZIP: 02109
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
C--> 26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/09/553,368
C--> 28 (B) FILING DATE: 20-Apr-2000
29 (C) CLASSIFICATION:
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US 60/067,614
33 (B) FILING DATE: 05 DECEMBER 1997
34 (A) APPLICATION NUMBER: US 60/071,596
35 (B) FILING DATE: 16 JANUARY 1998
36 (A) APPLICATION NUMBER: 09/205,817
37 (B) FILING DATE: 04 DECEMBER 1998
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: DOUROS, TIMOTHY J.
41 (B) REGISTRATION NUMBER: 41,716
42 (C) REFERENCE/DOCKET NUMBER: TTI-180DV
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (617)227-7400
46 (B) TELEFAX: (617)742-4214
48 (2) INFORMATION FOR SEQ ID NO: 1:
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 4374 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: cDNA
58 (ix) FEATURE:
59 (A) NAME/KEY: CDS
60 (B) LOCATION: 1..4374
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 ATG GAA ATA GAG CTC TCC ACC TGC TTC TTT CTG TGC CTT TTG CGA TTC

48

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65 Met Glu Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
66 1 5 10 15
68 TGC TTT AGT GCC ACC AGA AGA TAC TAC CTG GGT GCA GTG GAA CTG TCA 96
69 Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
70 20 25 30
72 TGG GAC TAT ATG CAA AGT GAT CTC GGA GAG CTG CCT GTG GAC GCA AGA 144
73 Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
74 35 40 45
76 TTT CCT CCT CGC GTG CCA AAA TCT TTT CCA TTC AAC ACC TCA GTC GTG 192
77 Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
78 50 55 60
80 TAC AAA AAG ACT CTG TTT GTA GAA TTC ACG GTT CAC CTT TTC AAC ATC 240
81 Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile
82 65 70 75 80
84 GCT AAG CCA AGG CCA CCC TGG ATG GGT CTG CTA GGT CCT ACC ATC CAA 288
85 Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
86 85 90 95
88 GCT GAG GTT TAT GAT ACA GTG GTC ATT ACA CTT AAG AAC ATG GCT TCC 336
89 Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
90 100 105 110
92 CAT CCT GTC TCC CTT CAT GCT GTT GGT GTA TCC TAC TGG AAA GCT TCT 384
93 His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
94 115 120 125
96 GAG GGA GCT GAA TAT GAT GAT CAG ACC AGT CAA AGG GAG AAA GAA GAT 432
97 Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
98 130 135 140
100 GAT AAA GTC TTC CCT GGT GGA AGC CAT ACA TAT GTC TGG CAA GTC CTG 480
101 Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
102 145 150 155 160
104 AAA GAG AAT GGT CCA ATG GCC TCC GAC CCA CTG TGC CTT ACC TAC TCA 528
105 Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
106 165 170 175
108 TAT CTT TCT CAT GTG GAC CTG GTT AAA GAC TTG AAT TCA GGC CTC ATT 576
109 Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
110 180 185 190
112 GGA GCC CTA CTA GTA TGT AGA GAA GGG AGT CTG GCC AAG GAA AAG ACA 624
113 Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
114 195 200 205
116 CAG ACC TTG CAC AAA TTT ATA CTA CTT TTT GCT GTA TTT GAT GAA GGG 672
117 Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
118 210 215 220
120 AAA AGT TGG CAC TCA GAA ACA AAG AAC TCC CTC ATG CAA GAT AGG GAT 720
121 Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
122 225 230 235 240
124 GCT GCA TCT GCT CGG GCC TGG CCT AAA ATG CAC ACA GTC AAT GGT TAT 768
125 Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
126 245 250 255
128 GTA AAC AGG AGC CTG CCA GGA CTG ATT GGA TGC CAC AGG AAA TCA GTC 816
129 Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val

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130		260		265		270	
132	TAT TGG CAT	GTT ATA GGA ATG GGC ACC ACT CCT GAA GTG CAC TCA ATA	864				
133	Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile						
134		275	280	285			
136	TTC CTC GAA GGA CAC ACA TTT CTT GTT AGA AAC CAT CGC CAG GCG TCC	912					
137	Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser						
138		290	295	300			
140	TTG GAA ATC TCG CCA ATA ACT TTC CTT ACT GCT CAA ACA CTC CTC ATG	960					
141	Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met						
142	305	310	315	320			
144	GAC CTT GGA CAG TTT CTA CTG TTT TGT CAT ATC TCT TCC CAC CAA CAT	1008					
145	Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His						
146		325	330	335			
148	GAT GGC ATG GAA GCT TAT GTC AAA GTA GAC AGC TGT CCA GAG GAA CCC	1056					
149	Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro						
150		340	345	350			
152	CAA CTA CGA ATG AAA AAT AAT GAA GAA GCG GAA GAC TAT GAT GAT GAT	1104					
153	Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp						
154		355	360	365			
156	CTT ACC GAT TCT GAA ATG GAT GTG GTC AGA TTT GAT GAT GAC AAC TCT	1152					
157	Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser						
158		370	375	380			
160	CCT TCC TTT ATC CAA ATT CGC TCA GTT GCC AAG AAG CAT CCT AAA ACT	1200					
161	Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr						
162	385	390	395	400			
164	TGG GTA CAT TAC ATT GCT GCT GAA GAG GAG GAC TGG GAC TAT GCT CCC	1248					
165	Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro						
166		405	410	415			
168	TTA GTC CTC GCC CCC GAT GAC AGA AGT TAT AAA AGT CAA TAT TTG AAC	1296					
169	Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn						
170		420	425	430			
172	AAT GGC CCT CAG CGG ATT GGA AGG AAG TAC AAA AAA GTC CGA TTT ATG	1344					
173	Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met						
174		435	440	445			
176	GCA TAC ACA GAT GAA ACC TTT AAG ACT CGT GAA GCT ATT CAG CAT GAA	1392					
177	Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu						
178		450	455	460			
180	TCA GGA ATC TTG GGA CCT TTA CTT TAT GGG GAA GTT GGA GAC ACA CTG	1440					
181	Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu						
182	465	470	475	480			
184	CTC ATT ATA TTT AAG AAT CAA GCA AGC AGA CCA TAT AAC ATC TAC CCT	1488					
185	Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro						
186		485	490	495			
188	CAC GGA ATC ACC GAT GTC CGT CCT TTG TAT TCA CGC AGA TTA CCA AAA	1536					
189	His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys						
190		500	505	510			
192	GGA GTA AAA CAT TTG AAG GAT TTT CCA ATT CTG CCC GGA GAA ATA TTC	1584					
193	Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe						
194		515	520	525			

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196	AAA	TAT	AAA	TGG	ACA	GTG	ACT	GTA	GAA	GAT	GGG	CCA	ACT	AAA	TCA	GAT	1632
197	Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	
198		530					535					540					
200	CCT	CGG	TGC	CTG	ACC	CGC	TAT	TAC	TCT	AGT	TTC	GTC	AAT	ATG	GAG	AGA	1680
201	Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg	
202	545					550				555					560		
204	GAT	CTA	GCT	TCA	GGA	CTC	ATT	GGC	CCT	CTC	CTC	ATC	TGC	TAC	AAA	GAA	1728
205	Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu	
206					565				570						575		
208	TCT	GTA	GAT	CAA	AGA	GGA	AAC	CAG	ATA	ATG	TCA	GAC	AAG	AGG	AAT	GTC	1776
209	Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	
210				580					585					590			
212	ATC	CTG	TTT	TCT	GTA	TTT	GAT	GAG	AAC	CGA	AGC	TGG	TAC	CTC	ACA	GAG	1824
213	Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	
214			595				600					605					
216	AAT	ATA	CAA	CGC	TTT	CTC	CCC	AAT	CCC	GCT	GGA	GTG	CAG	CTT	GAG	GAT	1872
217	Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	
218		610					615					620					
220	CCA	GAG	TTC	CAA	GCC	TCC	AAC	ATC	ATG	CAC	AGC	ATC	AAT	GGC	TAT	GTT	1920
221	Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	
222	625					630					635				640		
224	TTC	GAT	AGT	TTG	CAG	TTG	TCA	GTT	TGT	TTG	CAT	GAA	GTA	GCA	TAC	TGG	1968
225	Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	
226					645					650					655		
228	TAC	ATT	CTA	AGC	ATT	GGA	GCA	CAG	ACT	GAC	TTC	CTT	TCT	GTC	TTC	TTC	2016
229	Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	
230				660					665					670			
232	TCT	GGA	TAT	ACC	TTC	AAA	CAC	AAA	ATG	GTC	TAT	GAA	GAC	ACA	CTC	ACC	2064
233	Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	
234			675				680					685					
236	CTA	TTC	CCA	TTC	TCC	GGA	GAA	ACT	GTC	TTC	ATG	TCG	ATG	GAA	AAC	CCA	2112
237	Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	
238		690					695				700						
240	GGA	CTA	TGG	ATT	CTG	GGG	TGC	CAC	AAC	TCA	GAC	TTT	CGG	AAC	AGA	GGC	2160
241	Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	
242	705					710					715				720		
244	ATG	ACC	GCC	TTA	CTG	AAA	GTT	TCC	AGT	TGT	GAC	AAG	AAC	ACT	GGA	GAT	2208
245	Met	Thr	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	
246					725					730					735		
248	TAT	TAC	GAG	GAC	AGT	TAT	GAA	GAT	ATT	TCA	GCA	TAC	TTG	CTG	AGT	AAA	2256
249	Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	
250				740					745					750			
252	AAC	AAT	GCC	ATT	GAA	CCA	AGA	AGC	TTC	TCC	CAG	AAC	CCA	CCA	GTC	TTG	2304
253	Asn	Asn	Ala	Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Pro	Pro	Val	Leu	
254			755				760					765					
256	AAA	CGC	CAT	CAA	CGG	GAA	ATA	ACT	CGT	ACT	ACT	CTT	CAA	TCA	GAT	CAA	2352
257	Lys	Arg	His	Gln	Arg	Glu	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser	Asp	Gln	
258		770					775					780					
260	GAG	GAA	ATT	GAC	TAT	GAT	GAT	ACC	ATA	TCA	GTT	GAA	ATG	AAG	AAG	GAA	2400

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261	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	Met	Lys	Lys	Glu	
262	785					790					795					800	
264	GAT	TTC	GAC	ATT	TAT	GAT	GAG	GAT	GAA	AAT	CAG	AGC	CCC	CGC	AGC	TTT	2448
265	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	
266					805					810					815		
268	CAA	AAG	AAA	ACA	CGA	CAC	TAT	TTT	ATT	GCT	GCA	GTG	GAG	AGG	CTC	TGG	2496
269	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	
270				820					825					830			
272	GAT	TAT	GGG	ATG	AGT	AGC	TCC	CCA	CAT	GTT	CTA	AGA	AAC	AGG	GCT	CAG	2544
273	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	
274			835				840						845				
276	AGT	GGC	AGT	GTC	CCT	CAG	TTC	AAG	AAA	GTA	GTA	TTC	CAG	GAA	TTT	ACC	2592
277	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr	
278		850					855					860					
280	GAT	GGC	TCC	TTT	ACT	CAA	CCC	TTA	TAC	CGT	GGA	GAA	CTA	AAT	GAA	CAT	2640
281	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	
282	865				870					875					880		
284	TTG	GGA	CTC	CTG	GGG	CCA	TAT	ATA	AGA	GCA	GAA	GTT	GAA	GAT	AAT	ATC	2688
285	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	
286				885					890					895			
288	ATG	GTT	ACC	TTC	AGA	AAT	CAG	GCC	TCT	CGT	CCC	TAT	TCC	TTC	TAT	TCT	2736
289	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	
290			900				905					910					
292	TCC	CTC	ATA	TCA	TAT	GAG	GAA	GAT	CAG	AGG	CAA	GGA	GCA	GAA	CCT	AGA	2784
293	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	
294		915				920				925							
296	AAA	AAC	TTT	GTC	AAG	CCT	AAT	GAA	ACC	AAA	ACT	TAC	TTT	TGG	AAA	GTG	2832
297	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	
298		930				935				940							
300	CAA	CAT	CAT	ATG	GCA	CCC	ACT	AAA	GAT	GAG	TTT	GAC	TGC	AAA	GCC	TGG	2880
301	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	
302	945				950					955					960		
304	GCT	TAT	TTC	TCC	GAT	GTC	GAC	CTG	GAA	AAA	GAT	GTG	CAC	TCA	GGC	CTG	2928
305	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	
306				965					970					975			
308	ATT	GGA	CCC	CTT	CTG	GTC	TGC	CAC	ACC	AAC	ACA	CTG	AAC	CCT	GCT	CAT	2976
309	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	
310			980				985					990					
312	GGG	AGA	CAA	GTG	ACA	GTA	CAG	GAA	TTT	GCT	CTG	TTT	TTC	ACC	ATC	TTC	3024
313	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	
314		995				1000						1005					
316	GAT	GAG	ACC	AAA	AGC	TGG	TAC	TTC	ACT	GAA	AAT	ATG	GAA	AGA	AAC	TGC	3072
317	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	
318		1010				1015						1020					
320	AGG	GCT	CCC	TGC	AAT	ATC	CAG	ATG	GAA	GAT	CCC	ACT	TTT	AAA	GAG	AAT	3120
321	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys	Glu	Asn	
322	1025				1030					1035					1040		
324	TAT	CGC	TTC	CAT	GCA	ATC	AAT	GGC	TAC	ATA	ATG	GAT	ACA	CTA	CCT	GGC	3168
325	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr	Leu	Pro	Gly	

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L:1319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1391 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1395 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:1447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:1459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:1471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:1479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1487 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3